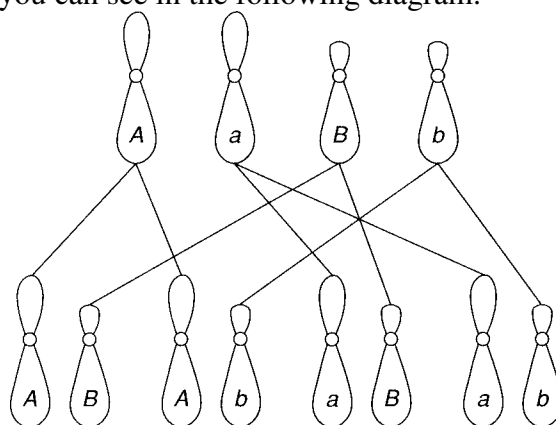


Name \_\_\_\_\_

## TWO FACTOR CROSSES

Crosses that involve two traits, such as pod color and pod shape, are called two-factor crosses. Predicting the outcome of two-factor crosses requires basically the same procedure as that for crosses involving one trait. Keep in mind that in two-factor crosses the genes controlling the two different traits are located on nonhomologous chromosomes. During meiosis, nonhomologous chromosomes assort independently. This means that each of the chromosomes of any pair of homologous chromosomes has an equal probability of ending up in a gamete with either chromosome from any other pair of homologous chromosomes. The genes that are located on nonhomologous chromosomes also assort independently, as you can see in the following diagram.



Because of independent assortment, a plant that is heterozygous for two traits (genotype AaBb) will produce equal numbers of four types of gametes - AB, Ab, aB, and ab.

In the example that follows, we will predict the results of a cross between two plants that are heterozygous for both pod color and pod shape.

### Sample Problem

Cross two pea plants that are heterozygous for pod color and pod shape and determine the phenotypic ratio of the offspring.

- Green pods (G) are dominant over yellow pods (g)
- Smooth pods (S) are dominant over constricted pods (s)

#### Step 1: Write the genotypes of the parents.

Since the parents are heterozygous for both traits, their genotype must be GgSs. The cross can be written as GgSs x GgSs.

#### Step 2: Determine the possible gametes that the parents can produce.

Each parent produces four types of gametes-GS, Gs, gS, and gs.

#### Step 3: Enter the possible gametes at the top and side of the Punnett square.

	GS	Gs	gS	gs
GS				
Gs				
gS				
gs				

**Step 4: Complete the Punnett square by writing the alleles from the gametes in the appropriate boxes.**

The alleles from the gamete above the box and the alleles from the gamete to the side of the box are combined inside each of the boxes. Write the capital letter first for each pair of alleles. The letters inside each box represent the probable genotypes of the offspring resulting from the cross.

	<i>GS</i>	<i>Gs</i>	<i>gS</i>	<i>gs</i>
<i>GS</i>	<i>GGSS</i>	<i>GGsS</i>	<i>GgSS</i>	<i>GgSs</i>
<i>Gs</i>	<i>GGsS</i>	<i>GGss</i>	<i>GgSs</i>	<i>Ggss</i>
<i>gS</i>	<i>GgSS</i>	<i>GgSs</i>	<i>ggSS</i>	<i>ggSs</i>
<i>gs</i>	<i>GgSs</i>	<i>Ggss</i>	<i>ggSs</i>	<i>ggss</i>

**Step 5: Determine the phenotypes of the offspring.**

In this example, 9/16 have green smooth pods, 3/16 have yellow smooth pods, 3/16 have green constricted pods, and 1/16 have yellow constricted pods (9:3:3:1).

**Now you try:**

1. Cross a homozygous yellow, homozygous constricted pod with a heterozygous green, heterozygous smooth pod.

♂ \_\_\_\_\_ x \_\_\_\_\_ ♀

Phenotypic ratio:

Probability offspring has  
green AND smooth pods: \_\_\_\_\_  
yellow AND constricted pods: \_\_\_\_\_


2. Cross a homozygous green, homozygous smooth pod with a heterozygous green, heterozygous smooth pod.

♂ \_\_\_\_\_ x \_\_\_\_\_ ♀

Phenotypic ratio:

Probability offspring has  
green AND smooth pods: \_\_\_\_\_  
yellow AND constricted pods: \_\_\_\_\_
